Figure 1

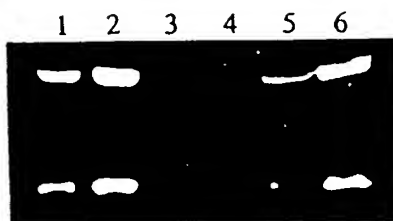## Figure 2

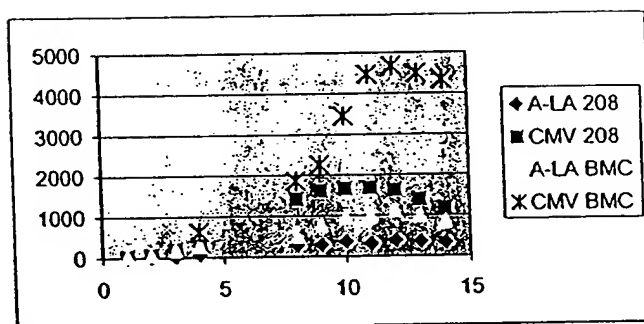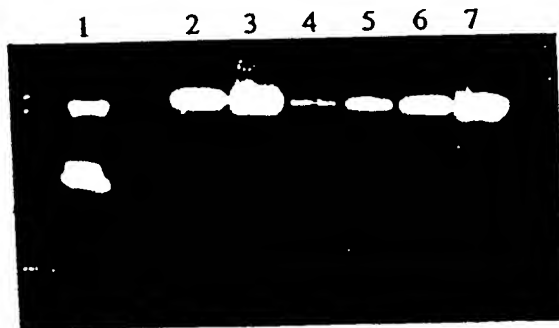## Figure 3

Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

```
   1    GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
  51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
 101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
 151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
 201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
 251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
 301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
 351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
 401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
 451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
 501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
 551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
 601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
 651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
 701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
 751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
 801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
 851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
 900    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
 951    ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001    CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051    TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101    CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151    CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201    CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251    GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301    GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351    ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401    CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451    TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501    TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551    TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601    TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651    AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701    ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751    CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801    GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851    GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901    AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951    CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001    GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051    GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101    C
```

1 - 1525	Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
1526 - 2056	Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
2057 - 2101	Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

```
1     GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51    ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101   GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151   GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201   AGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
```

1 - 119	Mutated PPE
120 -126	Linker
127 - 245	Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

```
1      GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51     CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551    ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601    TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651    GATATCTAGATCTCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

```
1     CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
51    TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
101   TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
151   ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
201   TATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC
251   CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATA
301   GTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACG
351   GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
401   CCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
451   TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
501   CATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTG
551   GATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC
601   AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCG
651   TAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGG
701   AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
751   CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801   CCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
851   CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
901   GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
951   TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
1001  CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051  ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101  AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151  TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201  AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
1251  GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
1301  CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351  GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
1401  CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
1451  TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551  CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
1601  GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
1651  AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
1701  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
1751  TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
1851  CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
1901  CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
2051  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
2101  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
2151  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201  ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251  GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTA
2301  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
2401  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
2451  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
2501  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
2551  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
2651  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
2701  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
2751  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
2801  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
```

Figure 7b

```
2851   CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
2901   GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
2951   TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
3001   TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
3051   TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
3101   TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
3151   TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
3201   GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
3251   CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
3301   GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
3351   GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
3401   CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
3451   CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
3501   CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
3551   TAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCC
3601   AGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCT
3651   TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGA
3701   GAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751   ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
3801   GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
3851   CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
3901   CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
3951   CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG ·
4001   CTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAC
4051   CCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCC
4101   GTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTG
4151   TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC
4201   TTTCATT
```

1 - 812	CMV promoter/enhancer
853-855	MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259	MN14 antibody heavy chain gene start codon
2271 - 2846	EMCV IRES
2847 - 2849	Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906	First codon mature MN14 antibody light chain gene
3543 - 3544	MN14 antibody light chain gene stop codon
3614 - 4207	MoMuLV 3' LTR

```
1     GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT
51    ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT
101   TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA
151   CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT
201   ATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
251   GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG
301   TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGG
351   TAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
401   CCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGT
451   ACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTC
501   ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG
551   ATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA
601   ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
651   AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
701   GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC
751   GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC
801   CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCAC
851   CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
901   TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT
951   GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG
1001  CTACTGGCTGCACTGGGTCAGGCAGGCACCTGGACAGGGTCTGGAATGGA
1051  TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC
1101  AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT
1151  GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAA
1201  GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC
1251  TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
1301  CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
1351  ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
1401  GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT
1451  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA
1501  TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
1551  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
1601  TGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG
1651  ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
1701  GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
1751  GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
1801  CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
1851  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
1901  CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
1951  ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG
2001  ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
2051  GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
2101  ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
2151  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT
2201  GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAAATGAA
2251  AGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAG
2301  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA
2351  TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC
2401  TTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGG
2451  TCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC
2501  AAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGC
2551  GACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA
2601  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
2651  TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAG
2701  AAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT
2751  TACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACG
2801  GGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT
```

Figure 8b

```
2851  CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901  AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC
2951  ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAATCACAA
3001  GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGC
3051  TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT
3101  GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC
3151  AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
3201  TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT
3251  GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTC
3301  TGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
3351  GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
3401  GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCT
3451  GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
3501  ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
3551  TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATT
3601  TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCA
3651  AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG
3701  AGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751  TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGC
3801  CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
3851  AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
3901  GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC
3951  CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
4001  GCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051  CCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCC
4101  GGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGG
4151  TCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG
4201  GTCTTTCATT
```

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

```
   1    CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCCTACACCTAGGGG
  51    AGAAGCAGCCAAGGGGTTGTTTCCCACCAAGGACGACCCGTCTGCGCACA
 101    AACGGATGAGCCCATCAGACAAAGACATATTCATTCTCTGCTGCAAACTT
 151    GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTCGTGC
 201    TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
 251    ATTACAATCTAAACAATTCGGAGAACTCGACCTTCCTCCTGAGGCAAGGA
 301    CCACAGCCAACTTCCTCTTACAAGCCGCATCGATTTTGTCCTTCAGAAAT
 351    AGAAATAAGAATGCTTGCTAAAAATTATATTTTTACCAATAAGACCAATC
 401    CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
 451    AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
 501    AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
 551    CAGGCCTAGAAGTAAAAAAGGGAAAAAAGAGTGTTTTTGTCAAAATAGGA
 601    GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
 651    AACAGATGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
 701    GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
 751    CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
 801    AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
 851    CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
 901    GCTGGACTAATAGAACATTATTCTGCAAAAACTTATGGCATGAGTTATTA
 951    TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001    TTTTGGTTACAAACTGTTCTTAAAACAAGGATGTGAGACAAGTGGTTTCC
1051    TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101    TTCCTATGTTCTTTTGGAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151    AACCAAGATATAAAAGAGTGCTGATTTTTTGAGTAAACTTGCAACAGTCC
1201    TAACATTCACCTCTTGTGTGTTTGTGTCTGTTCGCCATCCCGTCTCCGCT
1251    CGTCACTTATCCTTCACTTTCCAGAGGGTCCCCCCGCAGACCCCGGCGAC
1301    CCTCAGGTCGGCCGACTGCGGCAGCTGGCGCCCGAACAGGGACCCTCGGA
1351    TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCGTCTTGTTTTGT
1401    CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451    GAACCAAGCTAGCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501    TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551    GACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGA
1601    GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651    CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701    ACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCAC
1751    CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801    TCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851    GGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCAC
1901    ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951    TTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTA
2001    AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCT
2051    GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAA
2101    GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151    GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
2201    ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251    TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
2301    CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
2351    CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401    AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451    AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTG
2501    CCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAA
2551    AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601    GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
2651    GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
2701    ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAC
2751    TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801    AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
```

Figure 9b

```
2851    CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
2901    GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
2951    GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
3001    CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
3051    GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
3101    CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCG
3151    GGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTAC
3201    TGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT
3251    TTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC
3301    CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGG
3351    AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTT
3401    CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC
3451    CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
3501    ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTG
3551    TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG
3601    GATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTG
3651    CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCC
3701    CGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGC
3751    CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGG
3801    CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT
3851    GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT
3901    AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT
3951    GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGGT
4001    AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT
4051    CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAG
4101    GGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC
4151    TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTG
4201    CCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
4251    ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
4301    AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
4351    AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
4401    TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATCC
4451    CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA
4501    TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTT
4551    TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT
4601    TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC
4651    TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4701    CTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT
4751    CAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA
4801    ACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGG
4851    GCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGG
4901    CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA
4951    CGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGC
5001    CGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGG
5051    ATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGATA
5101    AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC
5151    CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT
5201    GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACA
5251    GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
5301    CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5351    ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
5401    GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
5451    GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG
5501    AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCC
5551    CGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCC
5601    GATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
5651    TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGT
5701    GATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 1457   Mouse mammary tumor virus LTR
1475 - 1726   Double mutated PPE sequence

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

```
   1    AAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
  51    AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCA
 101    GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
 151    CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
 201    AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAGAA
 251    CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
 301    CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
 351    TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCT
 401    CTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCT
 451    TCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
 501    CTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCT
 551    GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
 601    GATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAG
 651    CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
 701    ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGG
 751    CGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGG
 801    GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAA
 851    GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
 901    GACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGT
 951    TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001    TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051    CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGT
1101    CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151    TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201    GACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTT
1251    TTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCT
1301    GGGAAGCCTTGGCTTTTGACCCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351    CCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401    ACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451    CTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
1501    GTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTT
1551    GGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601    TCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTT
1651    TGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAG
1701    CGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTC
1751    GACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCC
1801    GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851    TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901    CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGAT
1951    GGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001    TCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051    GAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101    GGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGG
2151    CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201    CTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGC
2251    TCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301    GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351    CATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTC
2401    GGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451    CATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGTTGGT
2501    TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551    AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601    CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651    ATCCTAGAACTAGCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701    TGAGGAATACCGATTCTCTCATTAACATATTCAGGCCAGTTATCTGGGCT
2751    TAAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801    GAGGTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG
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Figure 10b
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2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCCAGGAGTTGGTA
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGACTGAACTGAACTGATAGTGTAATCCATGGTACAGA
3151 ATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTAAATTATTTACT
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATATAACCAATATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAATCTTGTTTTATA
3501 GGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGGCTTGGGAAGAT
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATTGCAAAGAG
3701 TTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGCATTGCAGAAAG
3801 ATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATACTGGAGTGGGT
3851 AGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAATTGAACTGGAG
3901 TCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTACCAGGTGGATA
3951 CTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCACCTTTCCCAAA
4001 AAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTTAG
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTTT
4201 TCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCATGCCTGGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGGAAGCTCGGTAT
4501 AGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTATATTGCCCCCAT
4551 GCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTCCCAGAACCAAC
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATTCTCTTCCTAGA
4801 TGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGGGCGCCGAATTC
4901 GAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT
5001 CGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
5051 AGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCA
5201 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
5301 TGGCCGGTCCCTGCCCTGTCCTGCTCCGGCATCTGGCTTCGATTTCACCA
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
5551 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
5601 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
5751 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
5851 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
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Figure 10c

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5951  GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
6001  AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
6051  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
6101  TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
6151  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
6201  CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
6251  CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
6301  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
6351  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
6451  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
6501  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
6551  ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
6601  GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
6651  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
6701  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
6751  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
6801  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
6851  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
6901  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
6951  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
7001  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
7051  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
7101  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
7151  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
7201  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
7251  GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
7301  TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
7351  TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
7401  TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
7451  TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501  TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
7551  GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
7601  CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
7651  GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
7701  GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
7751  CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
7801  CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
7851  CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
7901  CCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG
7951  ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
8001  TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC
8051  TTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT
8101  CTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
8151  ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
8201  TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGG
8251  AACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTG
8301  GGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTG
8351  GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCT
8401  ACGTCCCTTCGGCCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTG
8451  CCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCG
8501  GATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGAT
8551  AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACC
8601  CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCA
8651  TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAAC
8701  AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT
8751  CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA
8801  AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAAC
8851  AGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATC
8901  AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTT
8951  GAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCC
9001  CCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTC
```

Figure 10d

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9051  CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCA
9101  GTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAG
9151  TGATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

```
   1  GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
  51  AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
 101  ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
 151  GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
 201  AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
 251  GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
 301  CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
 351  AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
 401  AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
 451  AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
 501  ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
 551  GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
 601  CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
 651  CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
 701  GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
 751  CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
 801  ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
 851  ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
 901  ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
 951  ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101  ACTGGCAGGTGCTGGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151  CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201  AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251  GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301  TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC
2351  TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATGGAATGGAGCTG
2401  GGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCGACATCC
2451  AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501  ACTATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTA
2551  TCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA
2601  CCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
2651  CAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA
2701  TTACTGTCAACATTTTTGGAGTACTCCGTGGACGTTCGGTGGAGGCACCA
2751  AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
2801  CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
```

Figure 11b
2851 GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
2901 GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
2951 GACAGCACCTACAGCATGAGCAGCACCCTCACATTGACCAAGGACGAGTA
3001 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
3051 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT
3101 CCCCTGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAA
3151 GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC
3201 ATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTT
3251 CTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAG
3301 GTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA
3351 CAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGG
3401 CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA
3451 AGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501 GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCA
3551 GAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
3601 TTACATGTGTTTAGTCGAGGTTAAAAAAAACGTCTAGGCCCCCCGAACCAC
3651 GGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTG
3701 TCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT
3751 CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA
3801 GTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT
3851 GGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT
3901 CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC
3951 TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC
4001 TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAACTG
4051 GGGTTTCCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAA
4101 AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAA
4151 CTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
4201 CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251 CTTCCCAGCTGTCCTGCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA
4301 CTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCC
4351 CACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTG
4401 TACTAGTGGAGGTGGAGGTAGCCACCATCACCATCACCATTAATCTAGAG
4451 TTAAGCGGCCGTCGAGATCTCGACATCGATAATCAACCTCTGGATTACAA
4501 AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC
4551 TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
4601 ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTA
4651 TGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGT
4701 TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTC
4751 CTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT
4801 CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
4851 ACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTC
4901 GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCC
4951 TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTC
5001 TGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCC
5051 CTTTGGGCCGCCTCCCCGCCTGATCGATAAAATAAAAGATTTATTTAGT
5101 CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
5151 AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
5201 TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
5251 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
5351 GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
5401 AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
5451 GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
5501 CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
5551 CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
5601 ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC

Figure 11c

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5651   GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701   GGTCTTTCATT
```

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

```
1     TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51    TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101   GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151   GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201   GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251   AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301   TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
351   TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401   CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451   GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
501   CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
551   CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601   CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
651   TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701   TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751   CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
801   CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851   GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901   AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
951   CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001  TGCAGGTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATC
1051  AGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGA
1101  CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151  AATTTTCTAGGGGGAGCACCCACGTGTCCTGGCCAAAATTCGCAGTCCCC
1201  AACCTCCAATCACTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATC
1251  GCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTA
1301  TGCCTCATCTTCTTGTTGGTTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351  TTGTCCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401  CCTGCACGATTCCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTTGCTGT
1451  ACAAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTG
1501  GGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551  TCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACT
1601  GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTA
1651  CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTT
1701  GGGTATACATTTAAACCCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751  ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801  ATTGTACTAAAAATCAAGCAATGTTTTCGAAAACTGCCTGTAAATAGACC
1851  TATTGATTGGAAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901  CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951  ATACAATCTAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCT
2001  GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGGCAACGGTCAGGTC
2051  TCTGCCAAGTGTTTGCTGACGCAACCCCCACTGGATGGGGCTTGGCTATC
2101  GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151  GCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGGCGGTCTGGAGCGAAACT
2201  TATCGGCACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTC
2251  CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301  TTCGCTTTTGCATAGGGAGGGGGAAATGTAGTCTTATGCAATACACTTGT
2351  AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401  AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451  CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501  AATTCCGCATTGCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551  AAACGCCATTTTTGACCATTCACCACATTGGTGTGCACCTTCCAAAGCTT
2601  CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651  ACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAG
2701  CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751  TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801  ACAGCAAGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG
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Figure 12b

```
2851  GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT
2901  GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
2951  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
3001  GAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
3051  CCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
3101  ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT
3151  ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG
3201  TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
3251  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
3301  TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
3351  ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCC
3401  GGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
3451  AGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATC
3501  TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT
3551  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
3601  CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG
3651  GCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
3701  TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG
3751  ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
3801  AGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCG
3851  TTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
3901  GAGTTCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA
3951  TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
4001  ACTCAGCAATTCCAGCAGCTCCAAGCCGCAGTACAGGATGATCTCAGGGA
4051  GGTTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG
4101  AAGTTGTCCTACAGAATCGAAGGGGCCTAGACTTGTTATTTCTAAAAGAA
4151  GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA
4201  CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC
4251  AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT
4301  AACAGATCCCCTTGGTTTACCACCTTGATATCTACCATTATGGGACCCCT
4351  CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT
4401  TAGTCCAATTTGTTAAAGACAGGATATCAGTGTCCAGGCTCTAGTTTTG
4451  ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA
4501  ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
4551  CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
4601  AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGA
4651  TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
4701  GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC
4751  AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
4801  TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA
4851  TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
4901  CTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCG
4951  AGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
5001  TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
5051  GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGA
5101  TTGACTACCCGTCAGCGGGGGTCTTTCATT
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1 - 589	MoMuSV 5' LTR
659 - 897	Retroviral packaging region
1034 - 1714	Hepatitis B surface antigen
2279 - 2595	RSV promoter
2951 - 3745	Neomycin phosphotransferase gene
4537 - 5130	MoMuLV 3' LTR

```
1      GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTTACCATCTGAGCCCACCAGGGAAGCCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051   TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101   CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151   CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501   TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551   TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651   AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751   CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951   CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001   GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051   GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG
2101   GAATGGAGCTGGGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCA
2151   CTCCCAGGTTCAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG
2201   CTTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251   GCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG
2301   ATATTTTTCTCCCGGAAATGATGATTTTAAATACAATGAGAGGTTCAAGG
2351   GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG
2401   CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC
2451   CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
2501   GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT
2551   GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTCAGTTGGCGAGAAGGT
2601   TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA
2651   AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
2701   CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCAC
2751   AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA
2801   CTGAAGACCTGGCAGTTTATTACTGTCAGCAGTATTATAGCTATCCCCTC
```

Figure 13b

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2851  ACGTTCGGTGCTGGGACCAAGCTGGTGCTGAAACGGGCCGCCGAGCCCAA
2901  ATCTCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
2951  TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
3001  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
3051  CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
3101  ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151  GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA
3201  GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA
3251  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
3301  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCT
3351  GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401  GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
3451  GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
3501  GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551  ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGAGGCGGATCA
3601  GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACT
3651  GGAGCATTTACTGCTGGATTTACAGATGATTTTGAATGGAATTAATAATT
3701  ACAAGAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCC
3751  AAGAAGGCCACAGAACTGAAACATCTTCAGTGTCTAGAAGAAGAACTCAA
3801  ACCTCTGGAGGAAGTGCTAAATTTAGCTCAAAGCAAAAACTTTCACTTAA
3851  GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAG
3901  GGATCTGAAACAACATTCATGTGTGAATATGCTGATGAGACAGCAACCAT
3951  TGTAGAATTTCTGAACAGATGGATTACCTTTTGTCAAAGCATCATCTCAA
4001  CACTAACTTGAAGCTTGTTAACATCGATAAAATAAAAGATTTTATTTAGT
4051  CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
4101  AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
4151  TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
4201  CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
4251  AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
4301  GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351  AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
4401  GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
4451  CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
4501  CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
4551  ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC
4601  GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
4651  GGTCTTTCATT
```

1 - 2055   Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011   cc49-IL2 coding region
4068 - 4661   MoMuLV 3' LTR

```
1      GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051   TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101   CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151   CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501   TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551   TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651   AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751   CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951   CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001   GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051   GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101   ACTGGCAGGTGCTGGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151   CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201   AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251   GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301   TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351   CAGATCTAGGCCTCCTAGGTCGACGGATCCCCGGGAATTCGGCGCCGCCA
2401   CCATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451   ACCCAGGCCCAGGTCCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501   TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551   GCTACTATTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601   ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651   CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701   TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751   AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801   CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGAT
```

Figure 14b

```
2851  CTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC
2901  TATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAG
2951  CGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGA
3001  GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACC
3051  TGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101  GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC
3151  GGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTACTGG
3201  CCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT
3251  CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCT
3301  GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAAT
3351  GCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTT
3401  GAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCA
3451  CCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACC
3501  TGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551  AAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGAT
3601  GCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCAC
3651  ATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAAACGTCTAGGCCCCCCGA
3701  ACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTC
3751  CTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801  ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG
3851  AAGGTCACCATGACCTGCAGTGCCACCTCAAGTGTAAGTTACATACACTG
3901  GTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACAT
3951  CCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
4001  ACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC
4051  TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCGGTGCGGGGACCA
4101  AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
4151  CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
4201  GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
4251  GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
4301  GACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA
4351  TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
4401  CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT
4451  CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
4501  GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
4551  ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTC
4601  CTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
4651  TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACT
4701  GGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTT
4751  CCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCT
4801  GCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
4851  GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT
4901  TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGG
4951  ACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT
5001  CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCC
5051  TGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAAT
5101  GAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT
5151  GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
5201  TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
5251  AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT
5301  ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
5351  CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA
5401  GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTG
5451  CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCT
5501  TCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
5551  CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACC
5601  CTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCT
```

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

```
1     GGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51    CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101   TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151   ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251   CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301   AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351   GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401   AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451   GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501   ATGTGTTTAGTCGAGGTTAAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551   ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601   TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651   TCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

```
   1 TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
  51 TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
 101 GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
 151 GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
 201 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
 251 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
 301 TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
 351 TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
 401 CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
 451 GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
 501 CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
 551 CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
 601 CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
 651 TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
 701 TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
 751 CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
 801 CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
 851 GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
 901 AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
 951 CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATC
1001 GTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA
1051 GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG
1101 ATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGT
1151 TGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCC
1201 GCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
1251 TCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTG
1301 ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT
1351 ACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCC
1401 TTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTC
1451 ACTCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAG
1501 GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
1551 GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGG
1601 CTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTC
1651 TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAG
1701 GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
1751 GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG
1801 TGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTA
1851 TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC
1901 CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951 GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAG
2001 GGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGA
2051 CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA
2101 TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGT
2151 GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
2201 AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCG
2251 CCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
2301 TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAAC
2351 CTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGG
2401 CTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
2451 ATCTCATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGT
2501 TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA
2551 GTGCAAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCC
2601 ATGCCCCCGAACTGCAGGAGTGGGGGAGGCACGATGGCCGCTTTGGTCGAG
2651 GCGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCA
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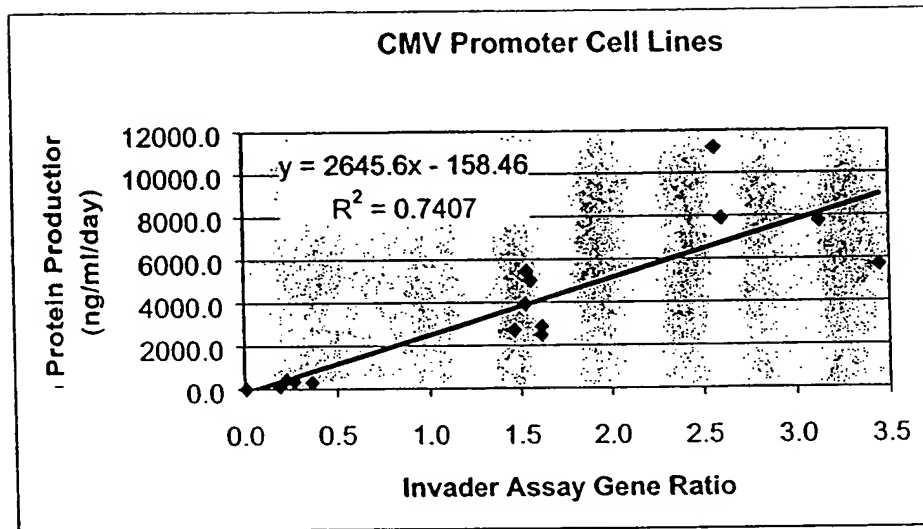
Figure 16b

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2801    GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT
2851    ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
2901    CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCAT
2951    AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC
3001    GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051    CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA
3101    GTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAG
3151    TCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGT
3201    GGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGT
3251    CAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
3301    GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGG
3351    GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
3401    ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451    GCCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGCCATC
3501    GATCCCGCCGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCCTGTC
3551    AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601    CCCTATCTGCATCTGTGGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651    GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC
3701    TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT
3751    CAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
3801    AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG
3851    TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG
3901    ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACA
3951    TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGA
4001    CATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCC
4051    TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101    AGCACCCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC
4151    CTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
4201    ACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTCC
4251    CTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
4301    GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT
4351    GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG
4401    TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451    AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC
4501    CTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCA
4551    AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCC
4601    ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC
4651    GTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG
4701    ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT
4751    TAAAAAAACGTCTAGGCCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGA
4801    AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA
4851    TCCTATTCCATGCCACCCAGGCCGAGGTTCAGCTTCAGCAGTCTGGGGCA
4901    GAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGG
4951    CTTCAACATTAAAGACACCTTTATGCACTGGGTGAAGCAGAGGCCTGAAC
5001    AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA
5051    TATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTC
5101    CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG
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5351    TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC
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5451    CCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAG
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5651    AAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA
5701    AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGA
5751    AGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAAC
5801    AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGGCCAAGAACAGA
5851    TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
```

Figure 16c

```
5901  GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951  CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
6001  GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT
6051  TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101  CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
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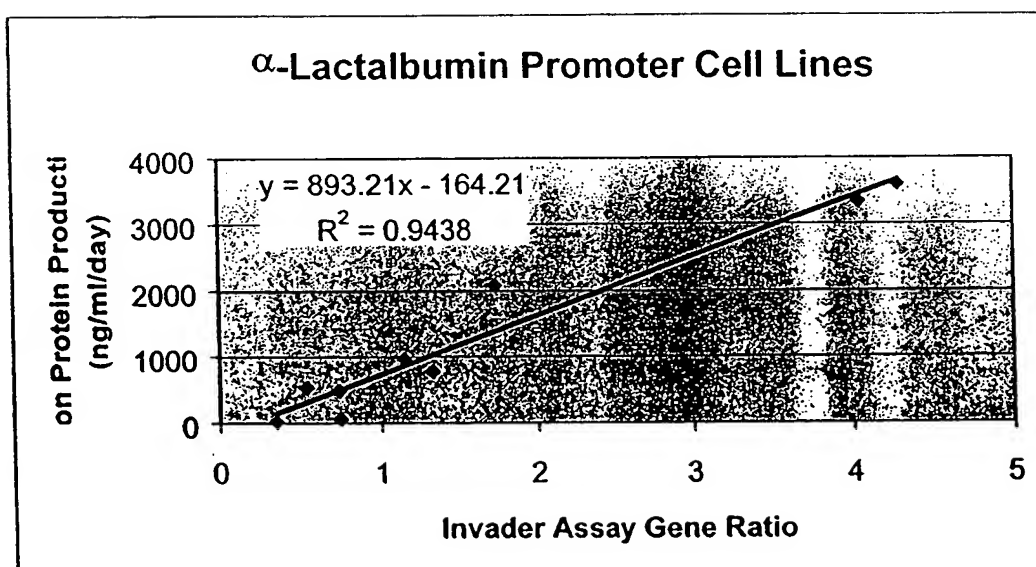
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Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α-LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17. CMV construct containing cell lines.

CMV Promoter Cell Lines

$y = 2645.6x - 158.46$

$R^2 = 0.7407$

Protein Production (ng/ml/day)

Invader Assay Gene Ratio

Figure 18: α-Lactalbumin construct containing cell lines

α-Lactalbumin Promoter Cell Lines

$y = 893.21x - 164.21$

$R^2 = 0.9438$

on Protein Producti (ng/ml/day)

Invader Assay Gene Ratio

```
   1   GAATTAATTCATACCAGATCACCGAAAACTGTCCTCCAAATGTGTCCCCC
  51   TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT
 101   TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT
 151   TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
 201   CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGT
 251   CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG
 301   TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG
 351   CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
 401   AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC
 451   ATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT
 501   ATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCG
 551   CTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGT
 601   CTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCT
 651   TGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCT
 701   CTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCC
 751   GGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
 801   AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTT
 851   TGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT
 901   GGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCT
 951   GGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGG
1001   AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG
1051   GAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCG
1101   GTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGT
1151   TCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG
1201   GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGAT
1251   GTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTG
1301   GGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC
1351   GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
1401   TTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGAC
1451   CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC
1501   ACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTT
1551   GAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
1601   TCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651   AGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC
1701   ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA
1751   CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA
1801   ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG
1851   CGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATC
1901   ATTTTACTGGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCT
1951   GCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2001   CAGGGGCATCTTGAGCCCCTGCGGACGGTGTCGACAGGTGCTTCTCGATC
2051   TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG
2101   GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA
2151   AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGAT
2201   TCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA
2251   CGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG
2301   CCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAAT
2351   AGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
2401   TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT
2451   TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501   AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2551   CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2601   ATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATAT
2651   TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT
2701   ATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACT
2751   AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATAT
2801   GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC
2851   CCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTA
```

Figure 19b

```
2901  ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
2951  AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC
3001  CTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTAC
3051  ATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCAT
3101  CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT
3151  AGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
3201  GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAA
3251  CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGG
3301  TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC
3351  CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT
3401  CCGCGGCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451  TTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG
3501  CTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
3551  GTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
3601  ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG
3651  GCCGCCAGTGTGCTGGAATTCACCATGGGGCAACCCGGGAACGGCAGCGC
3701  CTTCTTGCTGGCACCCAATGGAAGCCATGCGCCGGACCACGACGTCACGC
3751  AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC
3801  ATCGTCCTGGCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC
3851  CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAAGCTTGG
3901  CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGCCCTTTGGGGCCGCC
3951  CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG
4001  GACTTCCATTGATGTGCTGTGCGTCACGGCATCGATTGAGACCCTGTGCG
4051  TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG
4101  AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT
4151  TGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG
4201  CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC
4251  TTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCCTTCTA
4301  CGTTCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG
4351  CCAAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTC
4401  CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG
4451  CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG
4501  GCATCATCATGGGCACTTTCACCCTCTGCTGGCTGCCCTTCTTCATCGTT
4551  AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT
4601  CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCCTTATCT
4651  ACTGCCGGAGCCCAGATTTCAGGATTGCCTTCCAGGAGCTTCTGTGCCTG
4701  CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA
4751  CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAAATAAAC
4801  TGCTGTGTGAAGACCTCCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT
4851  ACTGTGCCTAGCGATAACATTGATTCACAAGGGAGGAATTGTAGTACAAA
4901  TGACTCACTGCTCTCGAGAATCGAGGGGCGGCACCACCATCATCACCACG
4951  TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC
5001  ACACTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA
5051  GGCCGGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
5101  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
5151  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
5201  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
5251  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
5301  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
5351  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
5401  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
5451  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
5501  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
5551  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
5601  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
5651  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
5701  GCCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG
5751  GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACA
5801  ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG
5851  CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT
5901  CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
5951  AGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCAG
```

Figure 19c

```
6001  ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC
6051  ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
6101  CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
6151  CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201  CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGA
6251  CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC
6301  ACCCATCAGGGCCTGAGATCGCCCGTCACAAAGAGCTTCAACAAGGGGAG
6351  AGTGTTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG
6401  CTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG
6451  TTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCCTCCTA
6501  GGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGG
6551  GGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601  ATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGAT
6651  CAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT
6701  GTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751  TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCT
6801  CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT
6851  CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC
6901  CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGC
6951  GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGG
7001  GGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAAT
7051  AAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAG
7101  GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGG
7151  GGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCAC
7201  CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACC
7251  TCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
7301  GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTG
7351  TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401  GCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC
7451  GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
7501  TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG
7551  GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT
7601  CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC
7651  AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC
7701  CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
7751  CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG
7801  CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT
7851  CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA
7901  GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC
7951  GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
8001  CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
8051  TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG
8101  CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
8151  GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
8201  AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG
8251  CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
8301  TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
8351  TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT
8401  AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451  CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA
8501  TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTA
8551  CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC
8601  TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA
8651  GTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG
8701  GAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC
8751  CATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT
8801  TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG
8851  TGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
8901  GTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTC
8951  TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA
9001  ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC
9051  GGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC
```

Figure 19d

```
9101  TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCG
9151  CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
9201  AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC
9251  AAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTC
9301  ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT
9351  CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG
9401  TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451  ATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCG
   1. TCTTCAAGAAT
```

Features:
```
149-737    Moloney murine sarcoma virus 5' LTR
807-1616   Extended Packaging Region
1680-1735  EM7 promoter (bacteriophage T7 promoter)
1754-2151  Blasticidin resistance gene coding sequence
2310-2440  SV40 poly A signal and site
2603-3420  CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646  IRES
5647-5703  Bovine a-lactalbumin signal peptide
5704-6372  'humanized' antibody light chain
6553-7146  MoMuLV 3' LTR
7683Origin of replication
9302-8442  b-Lactmase coding sequence
```

Figure 20
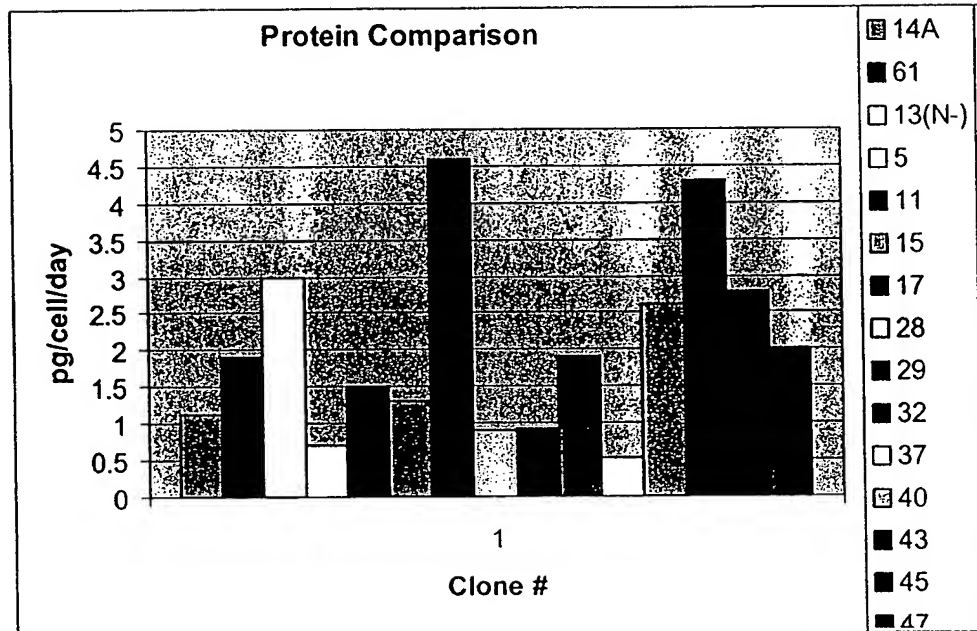
Figure 21(A). Gene Sequence of a Single Retrovector IgM Construct (SEQ ID NO:37)
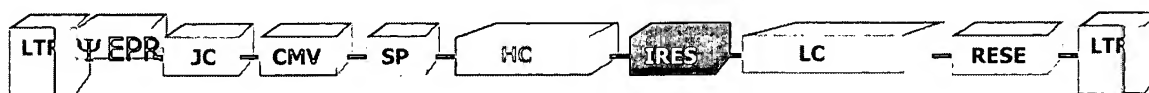
LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
JC =	J Chain Gene
CMV =	Simian Cytomegalovirus Promoter Region
SP =	Heavy Chain Signal Peptide
HC =	Mu Heavy Chain Gene
IRES =	Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
LC=	Kappa or Lambda Light Chain Gene
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

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GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAA
GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC
```

FIGURE 21(B)

CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCCGA
TCTGATCAAGAGACAGGATGAGAAGTCAAGATGAAGAACCATTTGCTTTTCTGGGGAGT
CCTGGCGGTTTTTATTAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTC
TTGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTTCCGAA
GATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCCTCTGAACAACAG
GGAGAATATCTCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTTGTCTG
ACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCT
ACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAG
AAACAAGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGG
AAACAGCCTTAACCCCAGATGCCTGCTATCCTGACTAAGATCCCTATGGCTATTGGCCA
GGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTTCCTAT
TGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCATATATGGGGCTTCCTAAT
ACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTATATATGGTCTTTCCTATT
GACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTGACGTCAATTAC
GGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCACCCACCATTGAC
GTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCTATTGACGTCAA
TGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAATAGTAACTTGGCAAGT
ACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGC
GGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGGAGGGGCA
ATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGT
CTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACGTCGGAGGAGCT
CGAAAGCTTAGGACCTCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACA
GCTACAGGTGTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCACATATTGGA
TGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGATTGGAGAAATTCATCCA
GATAGCAGTACGATTAACTATGCGCCGTCTCTAAAGGATAGATTTACAATATCGCGAGA
CAACGCCAAGAACACATTGTTCCTGCAAATGGACAGCCTGAGACCCGAAGACACCGGGG
TCTATTTTTGTGCAAGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGG
ACCCCGGTCACCGTCTCCTCAGGGAGTGCATCCGCCCCAACCCTTTTCCCCCTCGTCTC
CTGTGAGAATTCCCCGTCGGATACGAGCAGCGTGGCCGTTGGCTGCCTCGCACAGGACT
TCCTTCCCGACTCCATCACTTTGTCCTGGAAATACAAGAACAACTCTGACATCAGCAGT
ACCCGGGGCTTCCCATCAGTCCTGAGAGGGGGCAAGTACGCAGCCACCTCACAGGTGCT
GCTGCCTTCCAAGGACGTCATGCAGGGCACAGACGAACACGTGGTGTGCAAAGTCCAGC
ACCCCAACGGCAACAAAGAAAGAACGTGCCTCTTCCAGTGATTGCCGAGCTGCCTCCC
AAAGTGAGCGTCTTCGTCCCACCCCGCGACGGCTTCTTCGGCAACCCCCGCAAGTCCAA
GCTCATCTGCCAGGCCACGGGTTTCAGTCCCCGGCAGATTCAGGTGTCCTGGCTGCGCG
AGGGGAAGCAGGTGGGGTCTGGCGTCACCACGGACCAGGTGCAGGCTGAGGCCAAAGAG
TCTGGGCCCACGACCTACAAGGTGACCAGCACACTGACCATCAAAGAGAGCGACTGGCT
CGGCCAGAGCATGTTCACCTGCCGCGTGGATCACAGGGGCCTGACCTTCCAGCAGAATG
CGTCCTCCATGTGTGTCCCCGATCAAGACACAGCCATCCGGGTCTTCGCCATCCCCCCA
TCCTTTGCCAGCATCTTCCTCACCAAGTCCACCAAGTTGACCTGCCTGGTCACAGACCT
GACCACCTATGACAGCGTGACCATCTCCTGGACCCGCCAGAATGGCGAAGCTGTGAAAA
CCCACACCAACATCTCCGAGAGCCACCCCAATGCCACTTTCAGCGCCGTGGGTGAGGCC
AGCATCTGCGAGGATGACTGGAATTCCGGGGAGAGGTTCACGTGCACCGTGACCCACAC

FIGURE 21(C)

AGACCTGCCCTCGCCACTGAAGCAGACCATCTCCCGGCCCAAGGGGGTGGCCCTGCACA
GGCCCGATGTCTACTTGCTGCCACCAGCCCGGGAGCAGCTGAACCTGCGGGAGTCGGCC
ACCATCACGTGCCTGGTGACGGGCTTCTCTCCCGCGGACGTCTTCGTGCAGTGGATGCA
GAGGGGGCAGCCCTTGTCCCCGGAGAAGTATGTGACCAGCGCCCCAATGCCTGAGCCCC
AGGCCCCAGGCCGGTACTTCGCCCACAGCATCCTGACCGTGTCCGAAGAGGAATGGAAC
ACGGGGGAGACCTACACCTGCGTGGCCCATGAGGCCCTGCCCAACAGGGTCACCGAGAG
GACCGTGGACAAGTCCACCGGTAAACCCACCCTGTACAACGTGTCCCTGGTCATGTCCG
ACACAGCTGGCACCTGCTACTGAGATCTCTGCAGAAACCGGTCCTAGGTTTGGGAATTC
GCCCCTCTCCCTCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCC
GAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTC
TCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCCAGCTGACCCA
GAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACAGAGTGACCATCACCTGTAAGGCCA
GTCAGGATGTGGGTACTTCTGTAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAG
CTGCTGATCTACTGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAG
CGGTAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACATCGCCA
CCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAGGGACCAAGGTGGAA
ATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
AAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGATCTGTTAACCCTAGGCTCGAGTT
CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCT
ATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCT
TTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTG
ACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTC
GCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTG
GACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGT
CCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGC
TACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCT
GCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCG
CCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGA
AAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGC
TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAA

FIGURE 21(D)

GAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGC
CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCT
AGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTAT
TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCT
CAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGC
CCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCT
GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

Figure 22(A). Gene Sequence of a Double Retrovector IgM Heavy and Light Chain Construct (SEQ ID NO:38).
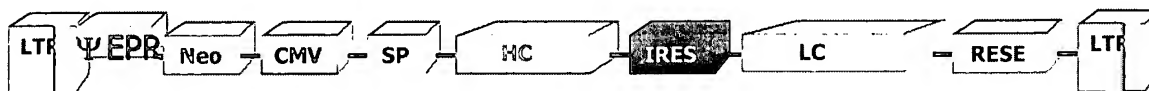
LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion

Ψ EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region

Neo = Neomycin Resistance Gene

CMV = Simian Cytomegalovirus Promoter Region

SP = Heavy Chain Signal Peptide

HC = Mu Heavy Chain Gene

IRES = Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide

LC= Kappa or Lambda Light Chain Gene

RESE = RNA Export and Stability Element

LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

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GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAA
```

FIGURE 22(B)

GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC
CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCCGA
TCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGC
AGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAA
TCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTT
GTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATC
GTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTT
GCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGA
TCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCG
CCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGT
GACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGAT
TCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACC
CGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGG
TATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
GAGGATCCCTATGGCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAG
TATTCCATATATGGGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCAT
ATACCATATATGGGGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGG
TCTCTATATATGGTCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGC
GCCTCCCCCATTGACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACG
TCAATAGGACCACCCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGT
TCTCACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATA
TCTATTAATAGTAACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGC
AGTACTCCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCC
CATTGACGTCAATGGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGG
CGGTAGGCGTGCCTAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATT
CTGCCTGGGGACGTCGGAGGAGCTCGAAAGCTTAGGACCTCACCATGGGATGGAGCTGT
ATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCGAGGTCCAACTGGTGGA
GAGCGGTGGAGGTGTTGTGCAACCTGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTG
GCTTCGATTTCACCACATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTT
GAGTGGATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTAAA
GGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCTGCAAATGGACA
GCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAAGCCTTTACTTCGGCTTCCCC
TGGTTTGCTTATTGGGGCCAAGGGACCCCGGTCACCGTCTCCTCAGGGAGTGCATCCGC
CCCAACCCTTTTCCCCCTCGTCTCCTGTGAGAATTCCCCGTCGGATACGAGCAGCGTGG
CCGTTGGCTGCCTCGCACAGGACTTCCTTCCCGACTCCATCACTTTGTCCTGGAAATAC
AAGAACAACTCTGACATCAGCAGTACCCGGGGCTTCCCATCAGTCCTGAGAGGGGGCAA
GTACGCAGCCACCTCACAGGTGCTGCTGCCTTCCAAGGACGTCATGCAGGGCACAGACG
AACACGTGGTGTGCAAAGTCCAGCACCCCAACGGCAACAAAGAAAAGAACGTGCCTCTT
CCAGTGATTGCCGAGCTGCCTCCCAAAGTGAGCGTCTTCGTCCCACCCCGCGACGGCTT
CTTCGGCAACCCCCGCAAGTCCAAGCTCATCTGCCAGGCCACGGGTTTCAGTCCCCGGC

FIGURE 22(C)

AGATTCAGGTGTCCTGGCTGCGCGAGGGGAAGCAGGTGGGGTCTGGCGTCACCACGGAC
CAGGTGCAGGCTGAGGCCAAAGAGTCTGGGCCCACGACCTACAAGGTGACCAGCACACT
GACCATCAAAGAGAGCGACTGGCTCGGCCAGAGCATGTTCACCTGCCGCGTGGATCACA
GGGGCCTGACCTTCCAGCAGAATGCGTCCTCCATGTGTGTCCCCGATCAAGACACAGCC
ATCCGGGTCTTCGCCATCCCCCCATCCTTTGCCAGCATCTTCCTCACCAAGTCCACCAA
GTTGACCTGCCTGGTCACAGACCTGACCACCTATGACAGCGTGACCATCTCCTGGACCC
GCCAGAATGGCGAAGCTGTGAAAACCCACACCAACATCTCCGAGAGCCACCCCAATGCC
ACTTTCAGCGCCGTGGGTGAGGCCAGCATCTGCGAGGATGACTGGAATTCCGGGGAGAG
GTTCACGTGCACCGTGACCCACACAGACCTGCCCTCGCCACTGAAGCAGACCATCTCCC
GGCCCAAGGGGGTGGCCCTGCACAGGCCCGATGTCTACTTGCTGCCACCAGCCCGGGAG
CAGCTGAACCTGCGGGAGTCGGCCACCATCACGTGCCTGGTGACGGGCTTCTCTCCCGC
GGACGTCTTCGTGCAGTGGATGCAGAGGGGGCAGCCCTTGTCCCCGGAGAAGTATGTGA
CCAGCGCCCCAATGCCTGAGCCCCAGGCCCCAGGCCGGTACTTCGCCCACAGCATCCTG
ACCGTGTCCGAAGAGGAATGGAACACGGGGGAGACCTACACCTGCGTGGCCCATGAGGC
CCTGCCCAACAGGGTCACCGAGAGGACCGTGGACAAGTCCACCGGTAAACCCACCCTGT
ACAACGTGTCCCTGGTCATGTCCGACACAGCTGGCACCTGCTACTGAGATCTCTGCAGA
AACCGGTCCTAGGTTTGGGAATTCGCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCC
GAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTG
CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCC
TAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAG
CAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAG
CGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCC
CATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAG
GTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACAC
GATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCAC
CCAGGCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACA
GAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGTAGCCTGGTACCAG
CAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTGGACATCCACCCGGCACACTGG
TGTGCCAAGCAGATTCAGCGGTAGCGGTAGCGGTACCGACTTCACCTTCACCATCAGCA
GCCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCG
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCG
GGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG
TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
ATCTGTTAACCCTAGGCTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTT
GTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCT
GCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTT
GTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTG
GCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACC
TGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT

FIGURE 22(D)

CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCG
TGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGG
ATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCC
TTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGA
CGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTA
GTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAA
GTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATC
AAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGG
ATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGAT
GCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGG
ACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGT
TCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTA
CCCGTCAGCGGGGGTCTTTCATT

Figure 23(A) Gene Sequence of a Double Retrovector IgM J Chain Construct (SEQ ID NO:39).
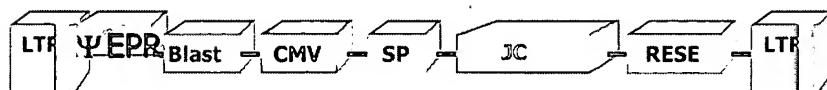
LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
Blast =	Blasticidin Resistance Gene
CMV =	Simian Cytomegalovirus Promoter Region
SP =	J Chain Signal Peptide
JC =	J Chain Gene
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

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GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAA
GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC
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FIGURE 23(B)

CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCATG
GCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAA
CAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCC
GCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTG
GTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGG
AAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATC
TGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGG
ATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTGGATCCCTATG
GCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCCATATATG
GGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCATATATGG
GGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTATATATGG
TCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTG
ACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCAC
CCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCT
ATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAATAGTA
ACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTG
ACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAAT
GGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCC
TAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACG
TCGGAGGAGCTCGAAAGCTTGAAGTCAAGATGAAGAACCATTTGCTTTTCTGGGGAGTC
CTGGCGGTTTTTATTAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTCT
TGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTTCCGAAG
ATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCCTCTGAACAACAGG
GAGAATATCTCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTTGTCTGA
CCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCTA
CCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAGA
AACAAGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGGA
AACAGCCTTAACCCCAGATGCCTGCTATCCTGACTAAGATCTGTTAACCGGTCCTAGGT
TTAAACTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTG
ACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCC
TTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCT
GGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCT
TTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCC
TTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGG
GACGTCCTTCTGCTACGTCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCC
TGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATC
TCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAA
AAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATT
TTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAA
CAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCC
GGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT

FIGURE 23(C)

AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGA
CCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
TGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGAC
TTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGG
GGGTCTTTCATT

FIGURE 24(A)

Mouse dihydrofolate reductase retrovector gene construct (SEQ ID NO:40).
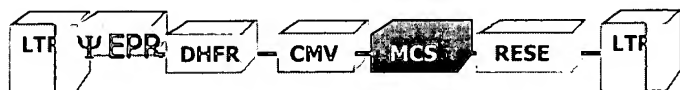
LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
             Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
             Packaging Region
DHFR =   Mouse Dihydrofolate Reductase Gene
CMV =   Simian Cytomegalovirus Promoter Region
MCS=   Multiple Cloning Site (Gene Insertion Site)
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

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  1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC
    ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
    CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCC
    AATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGG
    CAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAA
    TGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTA
    CATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATG
    GGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
    GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGC
    CCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
    AATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCC
    CGGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCT
    GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTG
    GGGGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
    TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTT
    ATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
    AACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGG
    GCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGA
    TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTT
    GCTTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
    TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTT
    ACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
    CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAA
    CCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTT
    AAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGT
    GACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTA
```

FIGURE 24(B)

AGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGATGACCTAGGCTTTTGCAAAAAGCTTTATCCCCGCTGCCA
TCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCCCAAGATATGGGGATTGGCAAG
AACGGAGACCTACCCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGAC
CACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGT
TCTCCATTCCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTTCTCAGTAGA
GAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGCCAAAGTTTGGATGATGCCTT
AAGACTTATTGAACAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAG
GCAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTCAGACTCTTTGTGACA
AGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTGGGGAAATA
TAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCA
AGTATAAGTTTGAAGTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCT
GCTCCCCTCCTAAAGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGAT
CCCTATGGCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCC
ATATATGGGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCA
TATATGGGGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTA
TATATGGTCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCC
CCCATTGACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATA
GGACCACCCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCAC
GCCCCCTATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATT
AATAGTAACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACT
CCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGA
CGTCAATGGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAG
GCGTGCCTAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCT
GGGGACGTCGGAGGAGCTCGAAAGCTTCTAGACAATTGACGCGTAGGCCTGCGGCCGCG
TCGACCAAGGGCCCAGATCTGTTAACCGGTCCTAGGTTTAAACTCGAGTTCGACATCGA
TAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTG
CTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCC
CGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGA
GTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCC
CCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCC
CTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGC
TCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTT
GGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCT
TCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCT
TCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGC
ATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACA
TAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGG
GCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATG
GAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCA
GGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCA

FIGURE 24(C)

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TCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAA
CCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAG
AGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACC
CGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGG
GAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT    4354
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1 - 763	HCMV-MOMUSV CHIMERIC 5'LTR
833 - 1642	EXTENDED PACKAGING REGION
1712 - 2272	MOUSE DHFR GENE CODING REGION
2355 - 3038	SIMIAN CMV PROMOTER
3029 - 3114	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3121 - 3721	RESE
3761 - 4354	3'LTR

Figure 25(A)

Glutamine synthase Retrovector gene construct (SEQ ID NO:41)
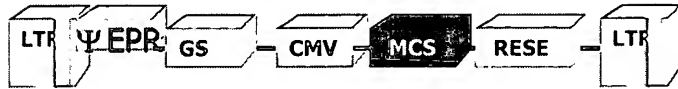
LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
                  Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
                  Packaging Region
DHFR =   Mouse Glutamine Synthase Gene
CMV =   Simian Cytomegalovirus Promoter Region
MCS=   Multiple Cloning Site (Gene Insertion Site)
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC
ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCC
AATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGC
CCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCC
CGGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCT
GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTG
GGGGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTT
ATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGG
GCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTT
GCTTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAA
CCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGT

FIGURE 25(B)

GACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTA
AGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGATGAACCATGGCCACCTCAGCAAGTTCCCACTTGAACAAA
GGCATCAAGCAAATGTACATGTCCCTGCCCCAGGGTGAGAAAGTCCAAGCCATGTATAT
CTGGGTTGATGGTACCGGAGAAGGACTGCGCTGCAAGACCCGTACCCTGGACTGTGAGC
CCAAGTGTGTGGAAGAGTTACCTGAGTGGAACTTTGATGGCTCTAGTACCTTTCAGTCT
GAAGGCTCCAACAGCGACATGTACCTCCATCCTGTTGCCATGTTTCGAGACCCCTTCCG
CAAAGACCCCAACAAGCTGGTGCTATGTGAAGTTTTCAAGTATAACCGGAAGCCTGCAG
AGACCAACTTGAGGCACATCTGTAAACGGATAATGGACATGGTGAGCAACCAGCACCCC
TGGTTTGGAATGGAGCAGGAATATACTCTTATGGGAACAGACGGCCACCCATTTGGTTG
GCCTTCCAATGGCTTCCCTGGACCCCAAGGCCCGTATTACTGCGGTGTGGGAGCAGACA
AGGCCTACGGCAGGGACATCGTGGAGGCTCACTACCGGGCCTGCTTGTATGCTGGAGTC
AAGATCACGGGGACAAATGCGGAGGTTATGCCTGCCCAGTGGGAATTCCAGATAGGACC
CTGTGAGGGGATCCGAATGGGAGATCATCTTTGGATAGCCCGTTTTATCTTGCATCGGG
TGTGCGAAGACTTTGGGGTGATAGCAACCTTTGACCCCAAGCCCATTCCAGGGAACTGG
AATGGTGCAGGCTGCCATACCAACTTCAGCACCAAGGCCATGCGGGAGGAGAATGGTCT
GAAGTGCATTGAGGAGGCCATTGACAAACTGAGCAAGAGGCACCAGTACCACATCCGCG
CCTACGATCCCAAGGGGGGCCTGGACAACGCCCGGCGTCTGACTGGATTCCACGAAACC
TCCAACATCAACGACTTTTCTGCCGGTGTTGCCAACCGCGGTGCCAGTATCCGCATTCC
CCGGACTGTCGGCCAGGAGAAGAAGGGCTACTTTGAAGACCGTCGGCCTTCTGCCAATT
GTGACCCCTATGCGGTGACAGAAGCCATCGTCCGCACGTGTCTCCTCAACGAAACAGGC
GACGAACCCTTCCAATACAAGAACTAAGGATCCCTATGGCTATTGGCCAGGTTCAATAC
TATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTTCCTATTGACGTAGAT
AGCCCCTCCCAATGGGCGGTCCCATATACCATATATGGGGCTTCCTAATACCGCCCATA
GCCACTCCCCCATTGACGTCAATGGTCTCTATATATGGTCTTTCCTATTGACGTCATAT
GGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTGACGTCAATTACGGTAAATGGC
CCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCACCCACCATTGACGTCAATGGGA
TGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCTATTGACGTCAATGACGGTAAA
TGGCCCACTTGGCAGTACATCAATATCTATTAATAGTAACTTGGCAAGTACATTACTAT
TGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGCGGTAAATGGC
CCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGGAGGGGCAATGACGCAAA
TGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGTCTATATAAGC
AATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACGTCGGAGGAGCTCGAAAGCTTC
TAGACAATTGACGCGTAGGCCTGCGGCCGCGTCGACCAAGGGCCCAGATCTGTTAACCG
GTCCTAGGTTTAAACTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTTGT
GAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGC
TTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGC
GTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCG
CCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTG
GTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT

FIGURE 25(C)

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TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTT
CCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACG
AGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGT
CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGT
AACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAA
GGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGT
TCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGAT
ATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGC
GGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTC
GCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCA
GTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACC
CGTCAGCGGGGGTCTTTCATT 4797
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1	-	763	HCMV-MOMUSV CHIMERIC 5'LTR
833	-	1642	EXTENDED PACKAGING REGION
1677	-	2795	MOUSE GLUTAMINE SYNTHASE GENE CODING REGION
2805	-	3472	SIMIAN CMV PROMOTER
3473	-	3558	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3565	-	4165	RESE
4205	-	4797	3'LTR